

OIPE

RAW SEQUENCE LISTING

DATE: 07/18/2001

PATENT APPLICATION: US/09/758,575

TIME: 12:43:17

Input Set : A:\517.app.txt

Output Set: N:\CRF3\07182001\I758575.raw

ENTERED

4 <110> APPLICANT: Kaufmann, Joerg
5 Harrowe, Greg
6 Reinhard, Christoph
7 Kang, Sammao
10 <120> TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN
11 BREAST CANCER
14 <130> FILE REFERENCE: 200130.517/1656.002
17 <140> CURRENT APPLICATION NUMBER: US 09/758,575
18 <141> CURRENT FILING DATE: 2001-01-09
20 <160> NUMBER OF SEQ ID NOS: 10
22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 2366
26 <212> TYPE: DNA
27 <213> ORGANISM: Homo sapiens
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31 gacggggggg gggattgaat gaaaagtga aaacacaggc tcgcagcgt ggagcccggg 120
32 gccgcggagc cgggccgggg cagcgccgtc tcgcctcgg ggccgcggg ggcgccctgc 180
33 tgagcgctac ccacgtgcgt ccgcgccacc tcgcgggcga cccgcggcc aaggcccccg 240
34 gcggagcggc tcccgggcgc cccgaactag cccccaactt tgggcgaagt ttgcctgcgc 300
35 ctctccccgc ccccagcgg cgcgcgggg ccgcggacgg cagcggcccc cggggatgcg 360
36 ccttccccgg gtacccttgg cgcgccctgc gctgctgctg ctgctgccgc tgctcgcgcc 420
37 gctgctggga acgggtgcgc cggccgagct gcgggtccgc gtgcggctgc cggacggcca 480
38 ggtgaccgag gagagcctgc aggcggacag cgacgcggac agcatcagcc tcgagctgcg 540
39 caagcccagc ggcacctcgc tctccttcac cgcgcacttc aagaaggatg tgaaggctct 600
40 ccgggccctg atcctggggg agctggagaa ggggcagagt cagttccagg cctctgctt 660
41 tgtcaccag ctgcagcaca atgagatcat cccagtgag gccatggcca agctccggca 720
42 gaaaaatccc cgggcagtgc ggcaggcgga ggaggttcgg ggtctggagc atctgcacat 780
43 ggatgtcgct gtcaacttca gccagggggc cctgctgagc ccccatctcc acaacgtgtg 840
44 tgccgaggcc gtggatgcca tctacaccgc ccaggaggat gtccggttct ggctggagca 900
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46 tcgctgcagg caggtggggg accgcgggaa gccctgcgtc tgccactatg gcctgagcct 1020
47 ggctggttac cctgcatgc tcaagtactg ccacagccgc gaccggccca cgcctacaa 1080
48 gtgtggcatc cgcagctgcc agaagagcta cagcttcgac ttctacgtgc ccagaggca 1140
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50 gctgctctgg gccactgct cttcaccagc cactagaggg ggtggcaacc cccactgag 1260
51 gccttatttc cctccctccc cactccctg gccctagagc ctgggcccct ctggccccat 1320
52 ctcacatgac tgtgaagggg gtgtggcatg gcagggggtc tcatgaaggc accccattc 1380
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56 acctccccag acacaactcc cttccccatg cacacatctg gaaggagctg gccctcagt 1620
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59 ggggcgagtg gagacctccc atcactgaga cagatcacag accacgagtg ccttccccg 1800
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61 tgtaagggttc tggggcaggg agggagcatg aagtacgagg aaaacttgaa ttccagattt 1920
62 ttaatgcaaa gtatttatca tttctaccag aaataaacgt tttaagtttt tacttgacta 1980
63 atgagaccca gagtttgagg aaaacttttg gccaatgctg ccacctgatg tcagaaagtg 2040
64 tccccacacc ctagcagtg cctatcttgg aacaagaact tcgaaagcac ctactgtgtg 2100
65 ctccagccatt tgaggaagga aggaggagaa ggaagatgtt actagggaag gatgagataa 2160
66 aacttctgca cccaagacaa tgagacagac ataactgcaa ccgtagtaag ccagtcagaa 2220
67 atagccagcg cgaaggcaag agatgggggtg gagattggaa ccccgcttca gatctgggct 2280
68 cggctactta cctgctgtgc agccatgggt caagttgctt gacctctctg tgccctccact 2340
69 cccttagcta taaaatgagc ttactt                                     2366

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71 <210> SEQ ID NO: 2

72 <211> LENGTH: 273

73 <212> TYPE: PRT

74 <213> ORGANISM: Homo sapiens

76 <400> SEQUENCE: 2

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78 1 5 10 15
79 Leu Pro Leu Leu Ala Pro Leu Leu Gly Thr Gly Ala Pro Ala Glu Leu
80 20 25 30
81 Arg Val Arg Val Arg Leu Pro Asp Gly Gln Val Thr Glu Glu Ser Leu
82 35 40 45
83 Gln Ala Asp Ser Asp Ala Asp Ser Ile Ser Leu Glu Leu Arg Lys Pro
84 50 55 60
85 Asp Gly Thr Leu Val Ser Phe Thr Ala Asp Phe Lys Lys Asp Val Lys
86 65 70 75 80
87 Val Phe Arg Ala Leu Ile Leu Gly Glu Leu Glu Lys Gly Gln Ser Gln
88 85 90 95
89 Phe Gln Ala Leu Cys Phe Val Thr Gln Leu Gln His Asn Glu Ile Ile
90 100 105 110
91 Pro Ser Glu Ala Met Ala Lys Leu Arg Gln Lys Asn Pro Arg Ala Val
92 115 120 125
93 Arg Gln Ala Glu Glu Val Arg Gly Leu Glu His Leu His Met Asp Val
94 130 135 140
95 Ala Val Asn Phe Ser Gln Gly Ala Leu Leu Ser Pro His Leu His Asn
96 145 150 155 160
97 Val Cys Ala Glu Ala Val Asp Ala Ile Tyr Thr Arg Gln Glu Asp Val
98 165 170 175
99 Arg Phe Trp Leu Glu Gln Gly Val Asp Ser Ser Val Phe Glu Ala Leu
100 180 185 190
101 Pro Lys Ala Ser Glu Gln Ala Glu Leu Pro Arg Cys Arg Gln Val Gly
102 195 200 205
103 Asp Arg Gly Lys Pro Cys Val Cys His Tyr Gly Leu Ser Leu Ala Trp
104 210 215 220
105 Tyr Pro Cys Met Leu Lys Tyr Cys His Ser Arg Asp Arg Pro Thr Pro
106 225 230 235 240
107 Tyr Lys Cys Gly Ile Arg Ser Cys Gln Lys Ser Tyr Ser Phe Asp Phe
108 245 250 255
109 Tyr Val Pro Gln Arg Gln Leu Cys Leu Trp Asp Glu Asp Pro Tyr Pro
110 260 265 270
111 Gly

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115 <210> SEQ ID NO: 3
116 <211> LENGTH: 30
117 <212> TYPE: PRT
118 <213> ORGANISM: Artificial Sequence
120 <220> FEATURE:
121 <223> OTHER INFORMATION: Putative signal peptide
123 <400> SEQUENCE: 3
124 Met Arg Leu Pro Gly Val Pro Leu Ala Arg Pro Ala Leu Leu Leu Leu
125 1 5 10 15
126 Leu Pro Leu Leu Ala Pro Leu Leu Gly Thr Gly Ala Pro Ala
127 20 25 30
130 <210> SEQ ID NO: 4
131 <211> LENGTH: 24
132 <212> TYPE: DNA
133 <213> ORGANISM: Artificial Sequence
135 <220> FEATURE:
136 <223> OTHER INFORMATION: Anti-sense oligonucleotide
138 <400> SEQUENCE: 4
139 agctgcggat gccacacttg tagg 24
141 <210> SEQ ID NO: 5
142 <211> LENGTH: 24
143 <212> TYPE: DNA
144 <213> ORGANISM: Artificial Sequence
146 <220> FEATURE:
147 <223> OTHER INFORMATION: Reverse control oligonucleotide
149 <400> SEQUENCE: 5
150 ggatgttcac accgtaggcg tcga 24
152 <210> SEQ ID NO: 6
153 <211> LENGTH: 273
154 <212> TYPE: PRT
155 <213> ORGANISM: Homo sapiens
157 <400> SEQUENCE: 6
158 Met Arg Leu Pro Gly Val Pro Leu Ala Arg Pro Ala Leu Leu Leu Leu
159 1 5 10 15
160 Leu Pro Leu Leu Ala Pro Leu Leu Gly Thr Gly Ala Pro Ala Glu Leu
161 20 25 30
162 Arg Val Arg Val Arg Leu Pro Asp Gly Gln Val Thr Glu Glu Ser Leu
163 35 40 45
164 Gln Ala Asp Ser Asp Ala Asp Ser Ile Ser Leu Glu Leu Arg Lys Pro
165 50 55 60
166 Asp Gly Ile Leu Val Ser Phe Thr Ala Asp Ile Lys Lys Asp Val Lys
167 65 70 75 80
168 Val Phe Arg Ala Leu Ile Leu Gly Glu Leu Lys Lys Gly Gln Ser Gln
169 85 90 95
170 Phe Gln Ala Leu Cys Phe Val Thr Gln Leu Gln His Asn Glu Ile Ile
171 100 105 110
172 Pro Ser Glu Ala Met Ala Lys Leu Arg Gln Lys Asn Pro Arg Ala Val
173 115 120 125
174 Arg Gln Ala Glu Glu Val Arg Gly Leu Glu His Leu His Met Asp Val

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175      130      135      140
176 Ala Val Asn Phe Ser Gln Gly Ala Leu Leu Ser Pro His Leu His Asn
177 145      150      155      160
178 Val Cys Ala Glu Ala Val Asp Ala Ile Val Thr Arg Gln Glu Asp Val
179      165      170      175
180 Arg Phe Trp Leu Glu Gln Gly Val Asp Ser Ser Val Phe Lys Ala Leu
181      180      185      190
182 Pro Lys Ala Ser Glu Gln Ala Glu Leu Pro Arg Cys Arg Gln Val Gly
183      195      200      205
184 Asp Arg Gly Lys Pro Cys Val Cys His Tyr Gly Leu Ser Leu Ala Trp
185      210      215      220
186 Val Pro Cys Met Leu Lys Val Cys His Ser Arg Asp Arg Pro Thr Pro
187 225      230      235      240
188 Val Lys Cys Gly Ile Arg Ser Cys Gln Lys Ser Tyr Ser Phe Asp Phe
189      245      250      255
190 Val Val Pro Gln Arg Gln Leu Cys Leu Trp Asp Glu Asp Pro Tyr Pro
191      260      265      270
192 Gly
196 <210> SEQ ID NO: 7
197 <211> LENGTH: 332
198 <212> TYPE: PRT
199 <213> ORGANISM: Drosophila melanogaster
201 <400> SEQUENCE: 7
202 Met Ile Leu Lys Glu Glu His Pro His Gln Ser Ile Glu Thr Ala Ala
203 1      5      10      15
204 Asn Ala Ala Arg Gln Ala Gln Val Arg Trp Arg Met Ala His Leu Lys
205      20      25      30
206 Ala Leu Ser Arg Thr Arg Thr Pro Ala His Gly Asn Cys Cys Gly Arg
207      35      40      45
208 Val Val Ser Lys Asn His Phe Lys His Ser Arg Ala Phe Leu Trp
209      50      55      60
210 Phe Leu Leu Cys Asn Leu Val Met Asn Ala Asp Ala Phe Ala His Ser
211 65      70      75      80
212 Gln Leu Leu Ile Asn Val Gln Asn Gln Gly Gly Glu Val Ile Gln Glu
213      85      90      95
214 Ser Ile Thr Ser Asn Ile Gly Glu Asp Leu Ile Thr Leu Glu Phe Gln
215      100      105      110
216 Lys Thr Asp Gly Ile Leu Ile Thr Gln Val Ile Asp Ile Arg Asn Glu
217      115      120      125
218 Val Gln Ile Leu Lys Ala Leu Val Leu Gly Glu Glu Lys Arg Gly Gln
219      130      135      140
220 Ser Gln Tyr Gln Val Met Cys Phe Ala Thr Lys Phe Asn Lys Gly Asp
221 145      150      155      160
222 Phe Ile Ser Ser Ala Ala Met Ala Lys Leu Arg Gln Lys Asn Pro His
223      165      170      175
224 Thr Ile Arg Thr Pro Glu Glu Asp Lys Gly Arg Glu Thr Phe Thr Met
225      180      185      190
226 Ser Ser Trp Val Gln Leu Asn Arg Ser Leu Pro Ile Thr Arg His Leu
227      195      200      205

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228 Gln Gly Leu Cys Ala Glu Ala Met Asp Ala Thr Val Val Arg Asp Val
 229 210 215 220
 230 Asp Leu Lys Ala Trp Ala Glu Leu Pro Gly Ser Ser Ile Ser Ser Leu
 231 225 230 235 240
 232 Lys Ala Ala Thr Glu Lys Phe Pro Asp Thr Leu Ser Thr Arg Cys Asn
 233 245 250 255
 234 Glu Val Ser Ser Leu Trp Ala Pro Cys Leu Cys Asn Leu Glu Thr Cys
 235 260 265 270
 236 Ile Gly Trp Val Pro Cys Gly Leu Lys Val Cys Lys Gly Lys Gly Val
 237 275 280 285
 238 Ala Gly Ala Asp Ser Ser Gly Ala Gln Gln Gln Ala Gln Pro Thr Asn
 239 290 295 300
 240 Val Arg Cys Gly Ile Lys Thr Cys Arg Lys Cys Thr Gln Phe Thr Tyr
 241 305 310 315 320
 242 Val Val Arg Gln Lys Gln Gln Cys Leu Trp Asp Glu
 243 325 330

246 <210> SEQ ID NO: 8

247 <211> LENGTH: 2366

248 <212> TYPE: DNA

249 <213> ORGANISM: Homo sapiens

251 <400> SEQUENCE: 8

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 253 gacggggggg gggattgaat gaaaagtgca aaacacaggc tcgcagcgct ggagcccggg 120
 254 gccgcggagc cgggccgggg cagcgccgct tccgcctcgg ggccgcgggg ggcgccctgc 180
 255 tgagcgctac ccacgtgcgt ccgcgccacc tcgcgggcca ccccgcgggc aaggcccccg 240
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 257 ctctccccgc ccccacgcgg cgcgcggggg ccgcggacgg cagcgggccc cggggatgcg 360
 258 ccttccccgg gtaccctctg cgcgcctctg gctgctgctg ctgctgcgcg tgctcgcgcc 420
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 260 ggtgaccgag gagagcctgc aggcggacac cgacgcggac agcatcagcc tcgagctgcg 540
 261 caagccccgc ggcaccctcg tctccttcac cgccgacttc aagaaggatg tgaaggtctt 600
 262 ccggggccctg atctggggg agctggagaa ggggcagagt cagttccagg cctctgctt 660
 263 tgtcacccag ctgcagcaca atgagatcat cccagtgag gccatggcca agctccggca 720
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VERIFICATION SUMMARY

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